

Package ‘muscle’

May 19, 2022

Type Package

Title Multiple Sequence Alignment with MUSCLE

Version 3.39.0

Date 2012-10-05

Author Algorithm by Robert C. Edgar. R port by Alex T. Kalinka.

Maintainer Alex T. Kalinka <alex.t.kalinka@gmail.com>

Description MUSCLE performs multiple sequence alignments of nucleotide or amino acid sequences.

biocViews MultipleSequenceAlignment, Alignment, Sequencing, Genetics, SequenceMatching, DataImport

Depends Biostrings

License Unlimited

URL <http://www.drive5.com/muscle/>

LazyLoad yes

LazyData yes

NeedsCompilation yes

git_url <https://git.bioconductor.org/packages/muscle>

git_branch master

git_last_commit 49ad052

git_last_commit_date 2022-04-26

Date/Publication 2022-05-19

R topics documented:

muscle-package	2
muscle	2
umax	4

Index	5
--------------	----------

muscle-package

Multiple Sequence Alignment

Description

MUSCLE performs multiple sequence alignments of nucleotide and amino acid sequences.

Details

Details about the algorithm can be found on the MUSCLE website:

<http://www.drive5.com/muscle/>

Author(s)

Algorithm: Robert C. Edgar

R port: Alex T. Kalinka <alex.t.kalinka@gmail.com>

References

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* **32**, 1792-1797.

See Also

[muscle](#), [umax](#)

Examples

```
## Align sequences in an XStringSet object.  
## Not run:  
aln <- muscle(stringset = umax)  
  
## End(Not run)
```

muscle

Multiple Sequence Alignment

Description

MUSCLE performs multiple sequence alignments of nucleotide or amino acid sequences.

Usage

```
muscle(stringset, quiet = FALSE, ...)
```

Arguments

stringset	An object of class <code>XStringSet</code> : <code>DNAStrngSet</code> , <code>RNAStringSet</code> , or <code>AAStringSet</code> .
quiet	Logical, whether to prevent printing of the progress of the algorithm to the screen. Defaults to <code>FALSE</code> .
...	Arguments (options and flags) for the MUSCLE algorithm (see Details).

Details

Arguments for the MUSCLE algorithm are either options or flags. Options take a variety of values, but flags are always logicals (`TRUE` or `FALSE`). All options and flags are explained in detail on the MUSCLE website: http://www.drive5.com/muscle/muscle_userguide3.8.html

Value

Output is an object of class `MultipleAlignment`: `DNAMultipleAlignment`, `RNAMultipleAlignment`, or `AAMultipleAlignment`.

Note

For further details see the MUSCLE website: <http://www.drive5.com/muscle/>

Author(s)

Algorithm by Robert C. Edgar. Ported into R by Alex T. Kalinka <alex.t.kalinka@gmail.com>

References

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* **32**, 1792-1797.

See Also

[umax](#)

Examples

```
## Align sequences in an XStringSet object.
aln <- muscle(stringset = umax)

## Switch on the diags flag.
aln <- muscle(stringset = umax, diags = TRUE)
```

umax

Unaligned MAX sequences

Description

Unaligned DNA sequences of the MAX gene for 31 mammalian species.

Usage

umax

Format

An object of class [DNAStrngSet](#).

Value

An object of class [DNAStrngSet](#).

Source

<http://www.ensembl.org/index.html>

References

Wagner, AJ et al. (1992) Expression, regulation, and chromosomal localization of the Max gene. *Proc Natl Acad Sci USA* **89**: 3111-3115.

Index

* datasets

umax, 4

AAMultipleAlignment, 3

AAStringSet, 3

DNAMultipleAlignment, 3

DNAStrngSet, 3, 4

MultipleAlignment, 3

muscle, 2, 2

muscle-package, 2

RNAMultipleAlignment, 3

RNAStringSet, 3

umax, 2, 3, 4

XStringSet, 3